FaMSA: Fast Multi-Scan Alignment with Partially Known Correspondences

Ernesto H. Teniente and Juan Andrade-Cetto
Institut de Robòtica i Informàtica Industrial, CSIC-UPC, Barcelona, Spain

***Abstract*— This paper presents FaMSA, an efficient method to boost 3D scan registration from partially known correspondence sets. This situation is typical at loop closure in large laser-based mapping sessions. In such cases, scan registration for consecutive point clouds has already been made during open loop traverse, and the point match history can be used to speed up the computation of new scan matches. FaMSA allows to quickly match a new scan with multiple consecutive scans at a time, with the consequent benefits in computational speed. Registration error is shown to be comparable to that of independent scan alignment. Results are shown for dense 3D outdoor scan matching.**

***Index terms* – ICP, 3D scan registration, scan alignment.**

Fig. 1. Dense point cloud registration during loop closure at the Barcelona Robot Lab.

I. Introduction

The Iterative Closest Point (ICP) algorithm is the de-facto standard for range registration in 3D mapping. It is used to compute the relative displacement between two robot poses by pairwise registration of the point clouds sensed from them. In a typical mapping session, consecutive pairwise registration is performed during open loop traverse, and accumulates drift error. This error is corrected by closing loops, i.e., matching point clouds with large temporal deviation (see Fig. 1).

Most SLAM algorithms keep probabilistic estimates of the robot location that can be used to determine whether or not a loop closure test is advisable. For instance, by considering not only pose uncertainty but information content as well [12]. But, once a loop closure test is deemed necessary, an algorithm that can compute it expeditiously is needed. Typically loop closure tests are checked not only from the current cloud to a query cloud in the past, but instead, to a consecutive set of query clouds in the past, which in turn have already been registered among them. Using this knowledge, we can expedite multiple registrations at a time. In this paper we propose FaMSA, a technique for fast multi-scan point cloud alignment at loop closure that takes advantage of the asserted point correspondences during sequential scan matching.

The paper is organized as follows. A description of related work is given in Section II. Section III details some implementation details of our ICP algorithms; and Section IV elaborates on the particularities of the method. Experiments that validate the viability of the method are given in Section VI, and Section VII contains some concluding remarks.

II. Related work

The most popular scan matching methods are based on the Iterative Closest Point algorithm [5]. The objective of this algorithm is to compute the relative motion between two data sets partially overlapped by minimizing the mean squared error of the distance between correspondences in the two sets.

In the original algorithm, a point-to-point metric is used to measure the distance between correspondences in the set. Point-to-plane metrics are also common practice [8], which make the method less susceptible to local minima. Furthermore, point-to-projection metrics are also possible [7], by matching points to ray indexes directly, inverting the ray casting process. A thorough account of these metrics and their properties is given in [21]. More recently, an error metric that weights unevenly rotation and translation was proposed for 2D [15], [16], and later extended to 3D [6]. The method uses point-to-projection minimization using triangles as the projection surface, and performs nearest neighbor search in the new metric space. FaMSA uses this metric for optimization.

ICP's computational bottleneck is in correspondence search. Most strategies to accelerate this search rely on some prior ordering of points within each point cloud, and use tree-based search methods such as the Approximate Nearest Neighbor [19], [3] that uses balanced kd-trees; kd-trees with caching mechanisms [24]; or parallelized kd-trees [18].

A method for fast NN search that competes with kd trees for execution speed is based on the spherical triangle constraint [10]. Like in [24], point caching is maintained from one iteration to the next, and ordering and triangle constraints are used to quickly identify correspondences. Aside from tree structures, other space partitioning mechanisms that allow for fast NN search include double z-buffering [4] and grid decomposition [26].

Point sampling is also a common strategy used to accelerate the matching process. Sampling however, only reduces asymptotic computational complexity by a constant factor. It is common practice to use hierarchical coarse-to-fine sampling methods to avoid missing fine resolution correspondences [25], [27]; and sampling can be either uniform [25], [7], random [14], or with ad-hoc reduction heuristics related to the sensing mechanism [20].

Outlier removal is also a major concern on most modern ICP implementations. Point rejection can be based on statistical point distributions [27], [14], [20], using fixed or dynamic distance thresholds [22], or using topological heuristics [25], [27], [22].

The idea of multi-scan alignment has been addressed as a bundle adjustment problem for 2D range scans [13] using force field simulation. The work that most relates to ours is the latent map [11], a multi-scan matching technique for 2D range matching.

III. Range image registration

A. Notation

The objective of the classic ICP algorithm is to compute the relative rotation and translation (R, t) between two partially overlapped point clouds P and Q, iteratively minimizing the mean square error over point matches. For a given set of point match indexes Y, ICP's cost function is

$$\arg\min_{R,t} \sum_{(i,j)\in Y} \|(p_i - Rq_j - t)\|^2 \ . \tag{1}$$

This minimization is solved iteratively, revising at each iteration the list of point matches, using for instance, NN search.

B. Implementation details and computational complexity

Correspondence search is the most expensive step in the ICP algorithm. Finding the NN to a given query point relies on the ability to discard large portions of the data with simple tests. Brute force correspondence search would take $O(n)$, with n the size of the point cloud. The preferred data structures used to solve the NN problem in low multidimensional spaces are kd-trees [9] with $O(n \log n)$ construction complexity and $O(\log n)$ search complexity. Box structures on the other hand take polynomial time to build [2] and constant time to search. Box structures are possible in ICP only when the initial and final poses do not change significantly so that NNs remain in the originally computed box.

We implement Acka's box search structure with some modifications. The box structure in [2] assigns to empty boxes the index of the last occupied box. We instead leave empty boxes out of the search. This serves effectively as a fixed distance filter with significant savings in computational load. Our method is faster than using the optimized Approximate Nearest Neigborh (ANN) library [3] with fixed radius search, as shown in the experiments section.

The original ICP algorithm of Besl and McKey [5] assumes that for each point in the reference set there must be a correspondence in the query set. In most applications this is not

FaMSA$(P, P', Q, Y, R, t, R_0, t_0)$
INPUTS:
- P, P': Two consecutive query point clouds.
- Q: Current point cloud.
- Y: Correspondences between P and P'.
- R, t: Relative displacement between P and P'.
- R_0, t_0: Initial displacement between P and Q.

OUTPUTS:
- R_P, t_P: Relative displacement between P and Q.
- $R_{P'}, t_{P'}$ Relative displacement between P' and Q.

$R_P, t_P \leftarrow R_0, t_0$
$R_{P'}, t_{P'} \leftarrow (R_0, t_0) \oplus (R, t)$
while not convergence **do**
  $Z \leftarrow$ NNSearch(P, Q, R_P, t_P)
  $Z' \leftarrow$ Link(Z, Y)
  $R_P, t_P \leftarrow$ ICPUpdate(P, Q, R_P, t_P, Z)
  $R_{P'}, t_{P'} \leftarrow$ ICPUpdate$(P', Q, R_{P'}, t_{P'}, Z')$
  convergence $\leftarrow (\epsilon < T)$ **and** $(\epsilon' < T)$
end while

Algorithm 1: FaMSA: Fast multi-scan alignment with partial known correspondences

the case and adequate similarity tests must be implemented. Using point distance as the only criteria for point similarity usually leads to wrong data association and local minima. We use, as in [22], oriented normal similarity constraints, together with statistical constraints [14], i.e, points at distances larger than a multiple of their standard deviation are rejected. These filtering strategies are time consuming, and should be used with discretion, since they require sorting and binary search. Correspondence uniqueness is also enforced and its implementation needs appropriate bookkeeping of matches at each iteration.

Several metrics exist to find the closest point during correspondence search [23], [21]. We adopt in this work the metric proposed in [6], but use point-to-point matching instead a point-to-triangle matching, and avoid the computational burden of computing the corresponding triangle mesh.

The metric is an approximated distance that penalizes rotations with a user defined weight L,

$$d(p_i, q_j) = \sqrt{\|p_i - Rq_j - t\|^2 - \frac{\|q_j \times (p_i - Rq_j - t)\|^2}{\|q_j\|^2 + L^2}} \ . \tag{2}$$

and a point norm $\|q\| = \sqrt{x^2 + y^2 + z^2 + L^2\theta^2}$. The metric d substitutes the Euclidean distance in Eq. 1, and as $L \to \infty$, this measure tends to the Euclidean distance.

IV. Fast multi scan alignment with partially known correspondences

Given that correspondence search is the most expensive part of any ICP implementation, we propose FaMSA to boost multiple scan alignment using previously known correspondences. That is, given two previously aligned point clouds P and P', the relative transformation between the two R, t, and a list Y of correspondences, we want to find the registration between the current point cloud Q and the two query scans P and P'.

FaMSA2($P, P', Q, Y, R, t, R_0, t_0$)

INPUTS:

P, P': Two consecutive query point clouds.
Q: Current point cloud.
Y: Correspondences between P and P'.
R, t: Relative displacement between P and P'.
R_0, t_0: Initial displacement between P and Q.

OUTPUTS:

R_P, t_P: Relative displacement between P and Q.
$R_{P'}, t_{P'}$ Relative displacement between P' and Q.

$R_P, t_P \leftarrow R_0, t_0$
while not convergence **do**
    $Z \leftarrow$ NNSEARCH(P, Q, R_P, t_P)
    $R_P, t_P \leftarrow$ ICPUPDATE(P, Q, R_P, t_P, Z)
    convergence $\leftarrow (\epsilon < T)$
end while
$R_{P'}, t_{P'} \leftarrow (R_P, t_P) \oplus (R, t)$
while not convergence **do**
    $Z' \leftarrow$ LINK(Z, Y)
    $R_{P'}, t_{P'} \leftarrow$ ICPUPDATE($P', Q', R_{P'}, t_{P'}, Z'$)
end while

Algorithm 2: FaMSA2: Very fast multi-scan alignment with partial known correspondences

The method proceeds as follows. Standard correspondence search is implemented between clouds P and Q, and for each match between points p_i and q_i, a link to P' is read from Y, and consequently the distance from q_j to p'_k is immediately established, avoiding the computation of similarity search and filters. Aside from the previous alignment of P and P', the method needs, as any other iterative ICP algorithm, an initial estimation of the relative displacement between the query cloud Q and P. Algorithm 1 shows the approach.

In the algorithm, Z and Z' indicate the correspondence sets between P and Q; and P' and Q, respectively. Appropriate index bookkeeping links to the other in constant time. The threshold T is used to indicate the maximum error allowed for the registration of both point clouds. The method also limits the search to a maximum number of iterations, typically set to 100.

The method is suboptimal in the sense that no new matches are sought for between point clouds P' and Q. For sufficiently close reference clouds P and P' it does not impose a limitation on the quality of the final correspondence.

In the same way that FaMSA takes advantage of the point correspondences between P and P' to boost the computation of the relative displacement between P' and Q, one can also defer the estimation of the pose between P' and Q until all iterations for P have finished and use the result as a starting point for the second optimization. This method is shown in Algorithm 2.

Extensive experimentation shows that only one iteration of ICP update suffices to revise the pose of P' with respect to Q, once the relative transformation between P and Q has been optimized. We call this method FaMSA2.

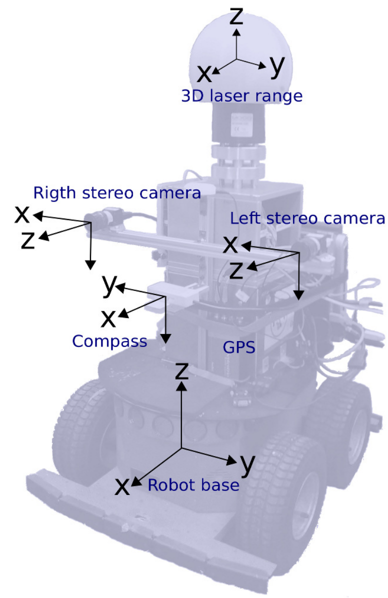


Fig. 2. Our mobile robotic platform.

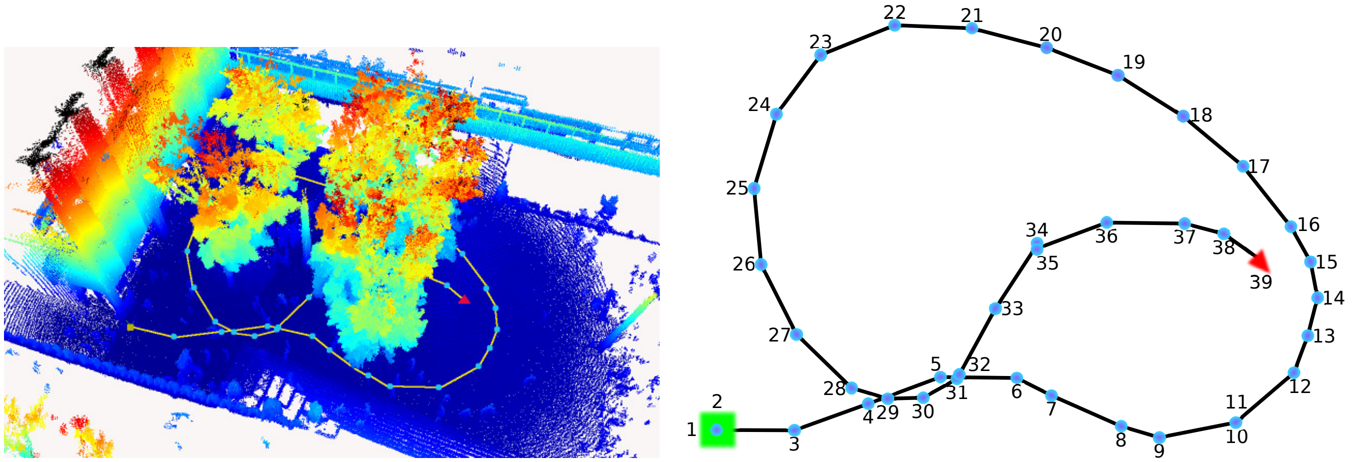
V. Experiment Setup

Our experimental data was acquired in the Barcelona Robot Lab, located at the Campus Nord of the Universitat Politècnica de Catalunya. The point clouds were captured using a Pioneer 3AT mobile robot and a custom built 3D laser with a Hokuyo UTM-30LX scanner mounted in a slip-ring. Each scan has 194,580 points with resolution of 0.5 deg azimuth and 0.25 deg elevation. Figure 2 shows the coordinate frames of all of our robot sensors. For the work reported here, only 39 scans from this dataset were used. Figure 7(a) shows a partial view of the mapped environment. The entire dataset is available in [1].

Each scan was uniformed sampled for faster convergence using voxel space discretization with a voxel size of 0.35 meters. During sampling, we also computed surface normals and enforced a minimum voxel occupancy restriction of 4 points. Random sampling with set sizes of 20 points was used for those boxes exceeding such number of points. Normal orientations are computed after random sampling. This has shown to produced better orientation estimates, especially around corners, when compared to other strategies such as k-NNs with density filtering.

ICP is executed in open loop for 39 consecutive scans, storing all relative pose displacements as well as the correspondence indexes. Then, a number of possible loop closure locations were selected manually. FaMSA was executed on these loop closure candidates. The specific parameters of the ICP implementation include: maximum angle between normals of 35 deg; upper and lower bounds of sigma rejection at 0.25σ and 5σ, respectively; and maximum number of iterations at 100.

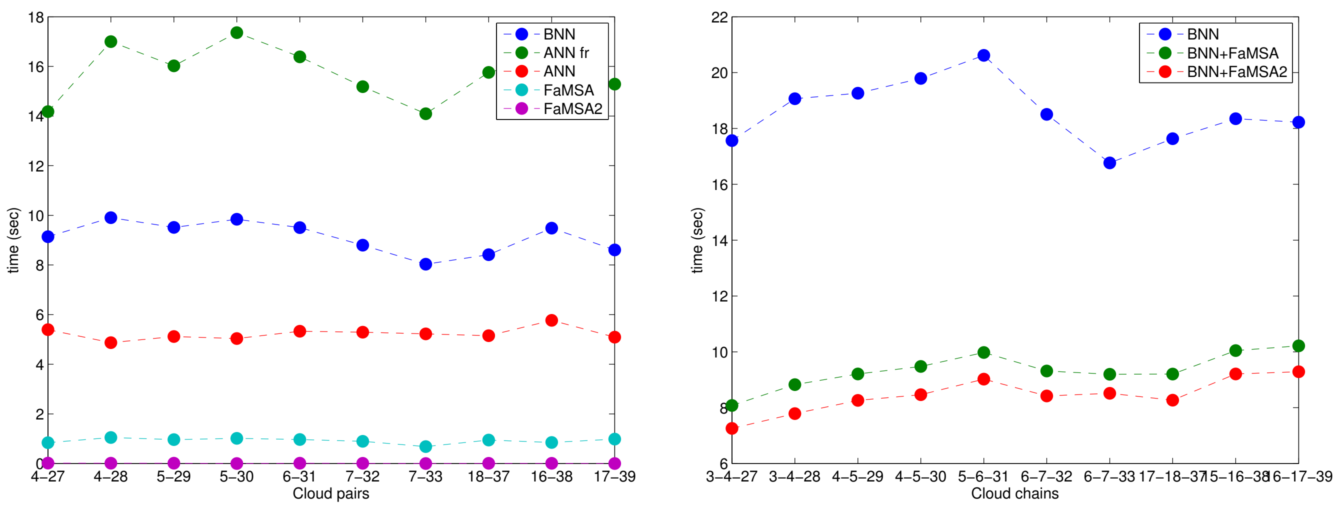
For the execution times reported, experiments were run in MATLAB using mex files of C++ routines in an Intel Core 2



(a) Dense point cloud registration. Color indicates height.

(b) Robot trajectory. In green the initial pose, in red the final pose.

Fig. 3. A path with 39 poses around the FIB plaza of the Barcelona Robot Lab.



(a) Time required to match Q and P', when the correspondences between P and P' are known.

(b) Time required to match Q with both P and P'.

Fig. 4. Algorithm performance.

Quad CPU Q9650 3.0 GHz system, with 4 GB RAM running Ubuntu 10.04 32 bits.

VI. Results

First, we compare the execution time in seconds for various implementations of multi-scan ICP. To this end, 10 loop closure locations Q are selected in the trajectory, and each is compared against its query clouds P and P'. Figure 4(a) shows the time it takes to align the current cloud Q to the second query cloud P' given the correspondences between Q and first cloud P are knwon. The methods BNN, ANN-FR and ANN refer to our implementation of voxel NNs; ANN with fixed radius, the size of the voxels; and conventional ANN. FaMSA and FaMSA2 stand for the methods presented in this paper that make use of previous point correspondence indexes to speed up registration. Note that FaMSA2 is the fastest of the methods, requiring only one iteration in the minimization. Extensive experimentation showed that further refinement in the case of FaMSA2 does not significantly improve the registration.

Figure 4(b) plots the time it takes to register the current point cloud Q against both query clouds P and P'. The plot shows individual registration using BNN and combined registration using the proposed schemes BNN+FaMSA and BNN+FaMSA2. The advantages in computational load of using the proposed mechanism are significative.

One might think that using only the correspondences in Y would yield suboptimal estimation. As a matter of fact, when using only this set to compute the relative displacement between P' and Q, the number of correspondences effectively halves (see Fig.5), but pose estimation accuracy does not suffer significantly.

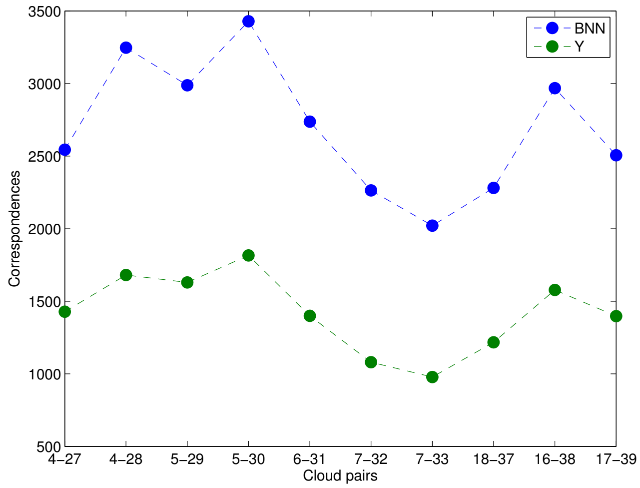


Fig. 5. Number of correspondences between P' and Q running a full BNN compared to using the stored set Y.

Figure 6 plots proportional translation and rotational errors as compared with full ICP estimation using BNN, and computed as follows [17]: using as ground truth the relative pose between Q and P' as computed with BNN (R_{BNN}, t_{BNN}), we measure the relative error of the estimated rotation (R, t), as $E_R(\%) = \|\mathbf{q}_{BNN} - \mathbf{q}\|/\|\mathbf{q}\|$, where $\mathbf{q}_{BNN}$ and $\mathbf{q}$ are the normalized quaternions of the corresponding orientation matrices R_{BNN} and R, respectively. Similarly, the relative error of the estimated translation is computed with $E_t(\%) = \|t_{BNN} - t_{P'}\|/\|t_{P'}\|$. Translation error turns out to be less than 0.7% for FaMSA and for all cloud pairs, and less than 0.2% for FaMSA2. Rotation error is barely noticable for both methods.

Figure 7 shows a sample of the point cloud match (best viewed in color). In blue, the current pose. In green and red, the query poses. A safe percentage of point cloud overlap in our method is roughly 50%. This is achieved with displacements of about 4 meters.

VII. Conclusions

This paper presents a novel ICP variation for simultaneous multiple scan registration that benefits from prior known correspondences. Speed up gain is substantial when compared with other methods.

The method uses a voxel structure to efficiently search for correspondences to the first cloud in the set, and a metric that unevenly weights rotation and translation.

The method was devised to search for loop closures after long sequences in open loop traverse but could be used for other configurations, provided the correspondences on the query set are known.

VIII. Acknowledgments

This work has been partially supported by the Mexican Council of Science and Technology with a PhD Scholarship to E.H. Teniente, by the Spanish Ministry of Science and Innovation under projects PAU (DPI2008-06022) and MIPRCV Consolider Ingenio (CSD2007-018), and by the CEEDS (FP7-ICT-2009-5-95682) and INTELLACT (FP7-ICT2009-6-269959) projects of the EU.

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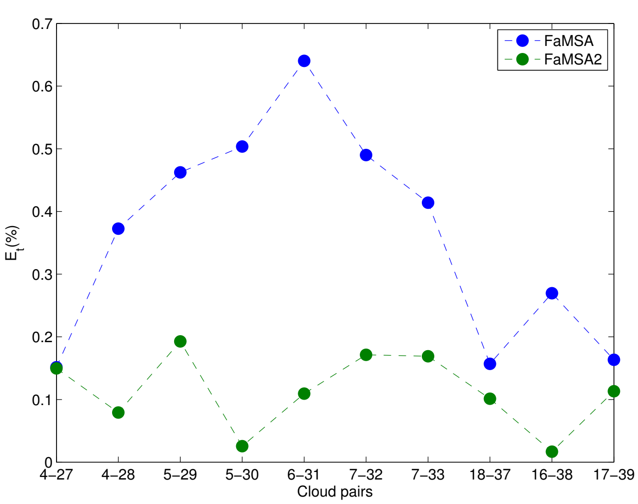
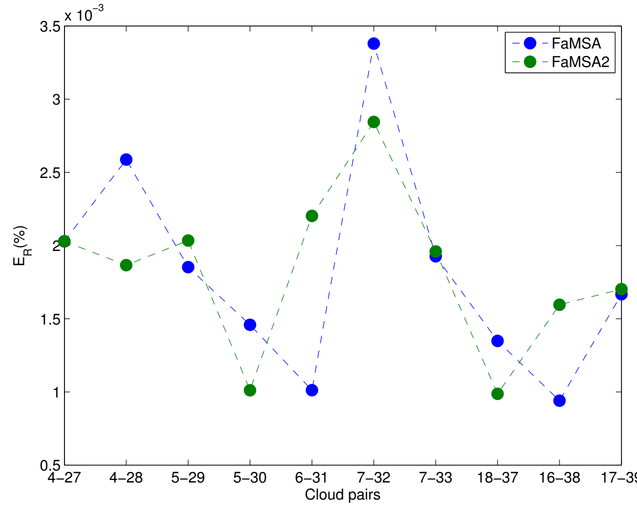
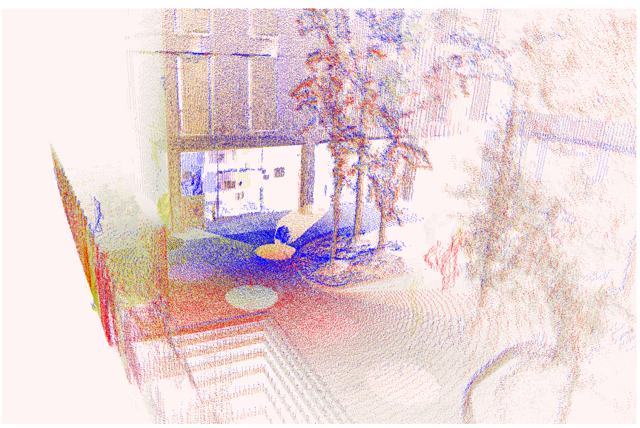


(a) Relative translational error.

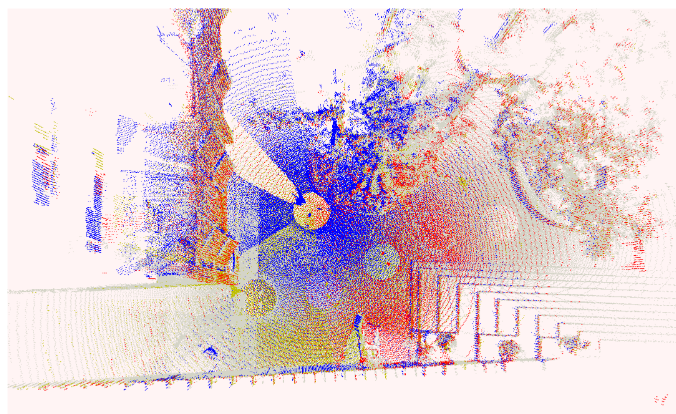


(b) Relative rotational error.

Fig. 6. Proportional translation and rotation errors for the registration between Q and P' with the proposed methods. BNN is used for ground truth comparison.



(a) P in yellow, P' in red, and Q in blue.



(b) Cenital view.

Fig. 7. A loop closure location between clouds 3, 4, and 28 in the BRL dataset (best viewed in color).

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